

Mail to  
Applicant

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/623,828

DATE: 06/14/2001  
TIME: 10:12:06

Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Schweighoffer, Fabien  
5 Bracco, Laurent  
6 Tocque, Bruno  
8 <120> TITLE OF INVENTION: Qualitative Differential Screening  
11 <130> FILE REFERENCE: 50146/004002  
13 <140> CURRENT APPLICATION NUMBER: 09/623,828  
14 <141> CURRENT FILING DATE: 2000-11-30  
16 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00547  
17 <151> PRIOR FILING DATE: 1999-03-11  
19 <160> NUMBER OF SEQ ID NOS: 16  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 23  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Artificial Sequence  
28 <220> FEATURE:  
29 <223> OTHER INFORMATION: Oligo  
31 <221> NAME/KEY: misc\_feature  
32 <222> LOCATION: 13-19, 23  
33 <223> OTHER INFORMATION: n = A,T,C or G  
35 <400> SEQUENCE: 1  
W--> 36 gagaagcgtt atnnnnnnna ggn 23  
38 <210> SEQ ID NO: 2  
39 <211> LENGTH: 24  
40 <212> TYPE: DNA  
41 <213> ORGANISM: Artificial Sequence  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: Oligo  
46 <221> NAME/KEY: misc\_feature  
47 <222> LOCATION: 13-20  
48 <223> OTHER INFORMATION: n = A,T,C or G  
50 <400> SEQUENCE: 2  
W--> 51 gagaagcgtt atnnnnnnnn tccc 24  
53 <210> SEQ ID NO: 3  
54 <211> LENGTH: 23  
55 <212> TYPE: DNA  
56 <213> ORGANISM: Artificial Sequence  
58 <220> FEATURE:  
59 <223> OTHER INFORMATION: Oligo  
61 <221> NAME/KEY: misc\_feature  
62 <222> LOCATION: (13)...(23)  
63 <223> OTHER INFORMATION: n = A,T,C or G  
65 <400> SEQUENCE: 3  
W--> 66 gagaagcgtt atnnnnnnnn nnn 23  
68 <210> SEQ ID NO: 4  
69 <211> LENGTH: 20  
70 <212> TYPE: DNA

Not a valid <223> response.  
What is the source of the  
genetic material making up  
the artificial sequences?  
See # 11 on the Error  
Summary Sheet.

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```

71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Oligo
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: (13)...(17)
78 <223> OTHER INFORMATION: n = A,T,C or G
80 <400> SEQUENCE: 4
W--> 81 gagaagcgtt atnnnnncca 20
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 66
85 <212> TYPE: DNA
86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 5
89 ccacacctgg ccagtatgtg ctactggct tgcagagtgg gcagccagcc taagcatttg 60
90 cactgg 66
92 <210> SEQ ID NO: 6
93 <211> LENGTH: 23
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Oligo
100 <400> SEQUENCE: 6
101 gggacctgtt tgacatgaag ccc 23
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 22
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Oligo
111 <400> SEQUENCE: 7
112 cagtttccgc tccacaggtt gc 22
114 <210> SEQ ID NO: 8
115 <211> LENGTH: 96
116 <212> TYPE: DNA
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 8
120 gtacgggaga gcacgaccac acctggccag tatgtgtca ctggcttgca gagtgggcag 60
121 cctaagcatt tgctactggt ggacctgag ggtgtg 96
123 <210> SEQ ID NO: 9
124 <211> LENGTH: 441
125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 9
129 Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly
130 1 5 10 15
131 Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn
132 20 25 30
133 Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro
134 35 40 45

```

See p. 1

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```

135 Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln
136      50                      55                      60
137 Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu
138 65                      70                      75                      80
139 Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr
140                      85                      90                      95
141 Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg
142      100                      105                      110
143 Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr
144      115                      120                      125
145 Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn
146      130                      135                      140
147 His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr
148 145                      150                      155                      160
149 Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala
150                      165                      170                      175
151 Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser
152      180                      185                      190
153 Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn
154      195                      200                      205
155 Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly
156      210                      215                      220
157 Ser Ala Trp Asp Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr
158 225                      230                      235                      240
159 Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met
160      245                      250                      255
161 Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro
162      260                      265                      270
163 Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln
164      275                      280                      285
165 Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro
166      290                      295                      300
167 Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val
168 305                      310                      315                      320
169 Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro
170      325                      330                      335
171 Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys
172      340                      345                      350
173 Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser
174      355                      360                      365
175 Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser
176      370                      375                      380
177 Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val
178 385                      390                      395                      400
179 Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr
180      405                      410                      415
181 His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys
182      420                      425                      430
183 Leu Gln Gln Pro Val Glu Arg Lys Leu

```

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TIME: 10:12:06

Input Set : A:\50146.004002.SEQLIST.TXT

Output Set: N:\CRF3\06142001\I623828.raw

184                    435                    440

187 <210> SEQ ID NO: 10

188 <211> LENGTH: 1326

189 <212> TYPE: DNA

190 <213> ORGANISM: Homo sapiens

192 <400> SEQUENCE: 10

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194 ggcgaggagt ggaccgcgca cgggagcttt gtcaataagc ccacgcgggg ctggctgcat 120

195 cccaacgaca aagtcatggg acccgggggt tcctacttgg ttcggtacat gggttgtgtg 180

196 gaggtcctcc agtcaatgcg tgccctggac ttcaacaccc ggactcagggt caccagggag 240

197 gccatcagtc tgggtgtgtg ggctgtgccc ggtgctaagg gggcgacaag gaggagaaaag 300

198 ccctgtagcc gcccgctcag ctctatcctg gggaggagta acctgaaatt tgctggaatg 360

199 ccaatcactc tcaccgtctc caccagcagc ctcaacctca tggccgcaga ctgcaaacag 420

200 atcatcgcca accaccacat gcaatctatc tcatttgcac ccggcgggga tccggacaca 480

201 gccgagtatg tcgcctatgt tgccaaagac cctgtgaatc agagagcctg ccacattctg 540

202 gagtgtcccg aagggtctgc ccaggatgtc atcagcacca ttggccaggc cttcgagttg 600

203 cgcttcaaac aatacctcag gaaccacccc aaactggtea cccctcatga caggatggct 660

204 ggctttgatg gctcagcatg ggatgaggag gaggaagagc cacctgacca tcagtactat 720

205 aatgacttcc cggggaagga accccccttg gggggggttg tagacatgag gottcgggaa 780

206 ggagcgcgtc caggggctgc tcgaccact gcacccaatg ccagacccc cagccacttg 840

207 ggagctacat tgctgttagg acagcctgtt gggggagatc cagaagtccg caaacagatg 900

208 ccacctccac caccctgtcc aggcagagag ctttttgatg atccctccta tgtcaacgtg 960

209 cagaacctag acaaggcccg gcaagcagtg ggtggtgctg ggccccccaa tcctgctatc 1020

210 aatggcagtg caccgcggga cctgtttgac atgaagccct tcgaagatgc tcttcgggtg 1080

211 cctccacctc ccagtcggt gtccatggct gagcagctcc gaggggagcc ctggttccat 1140

212 gggaaagctg gccggcgga ggctgaggca ctgctgcagc tcaatgggga cttcttggtt 1200

213 cggactaagg atcacgctt tgaaagtgtc agtcacctta tcagctacca catggacaat 1260

214 cacttgccca tcattctctg gggcagcgaa ctgtgtctac agcaacctgt ggagcggaaa 1320

215 ctgtga 1326

217 <210> SEQ ID NO: 11

218 <211> LENGTH: 19

219 <212> TYPE: DNA

220 <213> ORGANISM: Artificial Sequence

222 <220> FEATURE:

223 <223> OTHER INFORMATION: Oligo

225 <400> SEQUENCE: 11

226 tgcccaaata aacaagagc

228 <210> SEQ ID NO: 12

229 <211> LENGTH: 19

230 <212> TYPE: DNA

231 <213> ORGANISM: Artificial Sequence

233 <220> FEATURE:

234 <223> OTHER INFORMATION: Oligo

236 <400> SEQUENCE: 12

237 cccctgacaa gcctgaata 19

239 <210> SEQ ID NO: 13

240 <211> LENGTH: 24

241 <212> TYPE: DNA

242 <213> ORGANISM: Artificial Sequence

See p.1

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/623,828

DATE: 06/14/2001  
TIME: 10:12:06

Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

244 <220> FEATURE:  
245 <223> OTHER INFORMATION: (Oligo)  
247 <400> SEQUENCE: 13  
248 atgtctcaga gcaaccggga gctg 24  
250 <210> SEQ ID NO: 14  
251 <211> LENGTH: 24  
252 <212> TYPE: DNA  
253 <213> ORGANISM: Artificial Sequence  
255 <220> FEATURE:  
256 <223> OTHER INFORMATION: (Oligo)  
258 <400> SEQUENCE: 14  
259 gtggtccat tcaccgcggg gctg 24  
261 <210> SEQ ID NO: 15  
262 <211> LENGTH: 19  
263 <212> TYPE: DNA  
264 <213> ORGANISM: Artificial Sequence  
266 <220> FEATURE:  
267 <223> OTHER INFORMATION: (Oligo)  
269 <400> SEQUENCE: 15 19  
270 tgccaagaag ggaaggagt  
272 <210> SEQ ID NO: 16  
273 <211> LENGTH: 20  
274 <212> TYPE: DNA  
275 <213> ORGANISM: Artificial Sequence  
277 <220> FEATURE:  
278 <223> OTHER INFORMATION: (Oligo)  
280 <400> SEQUENCE: 16 20  
281 tgtcatgact ccagcaatag

*See p. 1*

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/623,828

DATE: 06/14/2001

TIME: 10:12:07

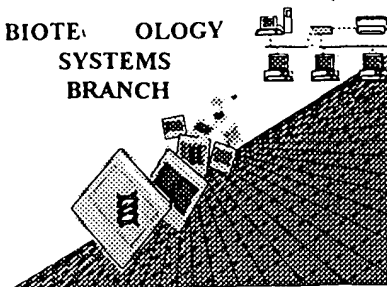
Input Set : A:\50146.004002.SEQLIST.TXT

Output Set: N:\CRF3\06142001\I623828.raw

L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



Mail to  
Applicant

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/623,828  
Source: 1656  
Date Processed by STIC: 6-14-01

RECEIVED  
JUL 09 2001  
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/623,828

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1      Wrapped Aminos
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 3      Numbering
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 6      "bug"
- 7      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
(OLD RULES)    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i)    SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
(NEW RULES)    <210> sequence id number  
                  <400> sequence id number  
                  000
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
Response    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                  is Artificial Sequence
- 11 ✓ Use of <220>    Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
"Unknown." (Please explain source of genetic material in <220> to <223> section.)  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file;  
"bug"    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.